

- 1 -

piece 1, NC\_000913, acpp\_fabF-, config: linear, direction: -, begin: 1151191, end: 1151055

5' t c c g g t c a c a a c t a c g a c g c t t a g a c a g t t t g t c c t a c a g g g a g g g a a a a a t g a t t c t a g v g g a c a c a a a a g a t a a a a g a t a a a a 3'  
 - ser - gly - his - asn - tyr - thr - thr - leu - arg - his - val - cys - pro - pro - gly - arg - glu - lys - met - ile - leu - val - gly - gln - lys - asp - lys -  
 - PRO - val - thr - thr - thr - ARG - ARG - leu - ASN - THR - Phe - VAL - LEU - GLN - GLV - LYS - LYS -  
 - PRO - Val - Thr - Thr - Thr - Arg - Arg - Leu - ASN - THR - Phe - Val - Leu - GLN - GLV - Lys - Lys -

...-----] NC\_000913.fabF

 sd  p35 2.6 bits

{- (10)-ir 1151137 Gap  
sd im 1151137.scrp 6ab

sd-ir 1151137 acpP fabF- total 8.5 bit

For more information about the study, please contact the study team at 1-800-258-4929 or visit [www.cancer.gov](http://www.cancer.gov).

51080 \* \*1151070 \* \*1151060 \*

Sequence logo showing the conservation of nucleotides across the alignment. The x-axis shows positions 11511110 through 1151060. The y-axis shows four bases: A (green), C (red), G (blue), and T (yellow). Conserved positions are indicated by vertical bars above the sequence.

...  p10 3.3 bits